

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claims 1-24 (canceled)

Claim 25 (withdrawn): An isolated nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, and a complement thereof.

Claim 26 (withdrawn): A nucleic acid fragment comprising at least a 20 contiguous base pair segment of the isolated nucleic acid sequence of claim 25.

Claim 27 (withdrawn): The nucleic acid fragment of claim 26 comprising a 20-30 contiguous base pair segment of the isolated nucleic acid sequence of claim 25.

Claim 28 (withdrawn): A primer comprising the nucleic acid fragment of claim 26.

Claim 29 (withdrawn): A probe comprising the nucleic acid fragment of claim 26.

Claim 30 (withdrawn): The isolated nucleic acid sequence of claim 25, wherein at least one preferred codon replaces at least one codon of said sequence.

Claim 31 (currently amended): An isolated amino acid sequence coded by the ~~isolated nucleic acid sequence of claim 25 nucleotides 112 to 462 of SEQ ID NO:11.~~

Claim 32 (currently amended): The isolated amino acid sequence of claim 31, wherein said isolated amino acid sequence is selected from ~~SEQ ID NO:23, SEQ~~

~~SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, and SEQ ID NO:42.~~

Claim 33 (currently amended): A An isolated peptide comprising at least a 10 contiguous amino acid segment of the isolated amino acid sequence of claim 32, wherein said contiguous amino acid segment comprises at least one contiguous amino acid from amino acids 37-117 of SEQ ID NO:32.

Claim 34 (currently amended): The isolated peptide of claim 33 comprising a 10-20 contiguous amino acid segment of the isolated amino acid sequence of claim 32.

Claim 35 (withdrawn): An expression vector comprising the isolated nucleic acid sequence of claim 25, said sequence operably-linked to control elements for the expression of said sequence in a host cell.

Claim 36 (withdrawn): A host cell transfected with the expression vector of claim 35.

Claim 37 (withdrawn): An antisense oligonucleotide comprising a 10-40 contiguous base pair segment of a reverse complement of a nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, and SEQ ID NO:21.

Claim 38 (withdrawn): A method for detecting the presence of at least one variant nucleic acid sequence of obesity and/or diabetes related genes in a biological sample comprising the steps of:

- (a) hybridizing to nucleic acid material of the biological sample an isolated nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ

ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, or a complement thereof; and

(b) detecting a hybridization complex produced by step (a);

wherein the presence of the hybridization complex correlates with the presence of at least one variant nucleic acid sequence in the biological sample.

**Claim 39 (withdrawn):** A method for determining the level of variant nucleic acid sequences in a biological sample comprising the steps of:

(a) hybridizing to nucleic acid material of the biological sample an isolated nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, or a complement thereof;

(b) determining the amount of hybridization complexes produced by step (a); and

(c) normalizing the amount of hybridization complexes to provide a level of variant nucleic acid sequences in the biological sample.

**Claim 40 (withdrawn):** A method for determining the ratio between the level of a nucleic acid sequence of an obesity and/or diabetes related gene variant in a first biological sample and a variant produced by alternative splicing in a second biological sample comprising the steps of:

(a) determining the level of a first nucleic acid sequence of an obesity and/or diabetes related gene variant in a first biological sample;

(b) determining the level of a second nucleic acid sequence of an alternative splicing form of the variant in a second biological sample; and

(c) comparing the levels obtained in step (a) and step (b) to give a ratio.

**Claim 41 (withdrawn):** The method of claim 40, wherein the first biological sample and the second biological sample are the same sample.

**Claim 42 (withdrawn):** The method of claim 40, wherein the first nucleic acid sequence and the second nucleic acid sequence are mRNA transcripts.

Claim 43 (withdrawn): The method of claim 42, wherein the first nucleic acid sequence and the second nucleic acid sequence are deposited on a nucleic acid chip.

Claim 44 (withdrawn): A method for the identification of compounds capable of affecting the binding affinity of obesity and/or diabetes related proteins to the receptors of said proteins comprising the steps of:

- (a) providing an amino acid sequence selected from SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, and SEQ ID NO:42;
- (b) contacting a candidate compound with the amino acid sequence in the presence of at least one receptor of an obesity and/or diabetes related gene;
- (c) determining the effect of the candidate compound on the binding of the amino acid sequence to the at least one receptor; and
- (d) selecting a compound capable of affecting the binding affinity of obesity and/or diabetes related proteins to the receptors of said proteins.

Claim 45 (withdrawn): A method for determining the ratio between the level of an obesity and/or diabetes related protein variant in a first biological sample and a variant produced by alternative splicing in a second biological sample comprising the steps of:

- (a) determining the level of a first amino acid sequence of an obesity and/or diabetes related gene variant in a first biological sample;
- (b) determining the level of a second amino acid sequence of an alternative splicing form of the variant in a second biological sample; and
- (c) comparing the levels obtained in step (a) and step (b) to give a ratio.

Claim 46 (withdrawn): A method of detecting a specific obesity and/or diabetes related nucleic acid sequence by polymerase chain reaction comprising the steps of:

- (a) amplifying a specific obesity and/or diabetes related nucleic acid sequence with a primer pair, wherein at least one of the primers comprises an at least 20 contiguous base pair segment of a nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, and a complement thereof; and
- (b) detecting the nucleic acid product of step (a).

Claim 47 (new): An isolated amino acid sequence having 90% identity with the amino acid sequence of claim 31.

Claim 48 (new): An isolated amino acid sequence coded by a nucleotide sequence having 90% identity to nucleotides 112 to 462 of SEQ ID NO:11.